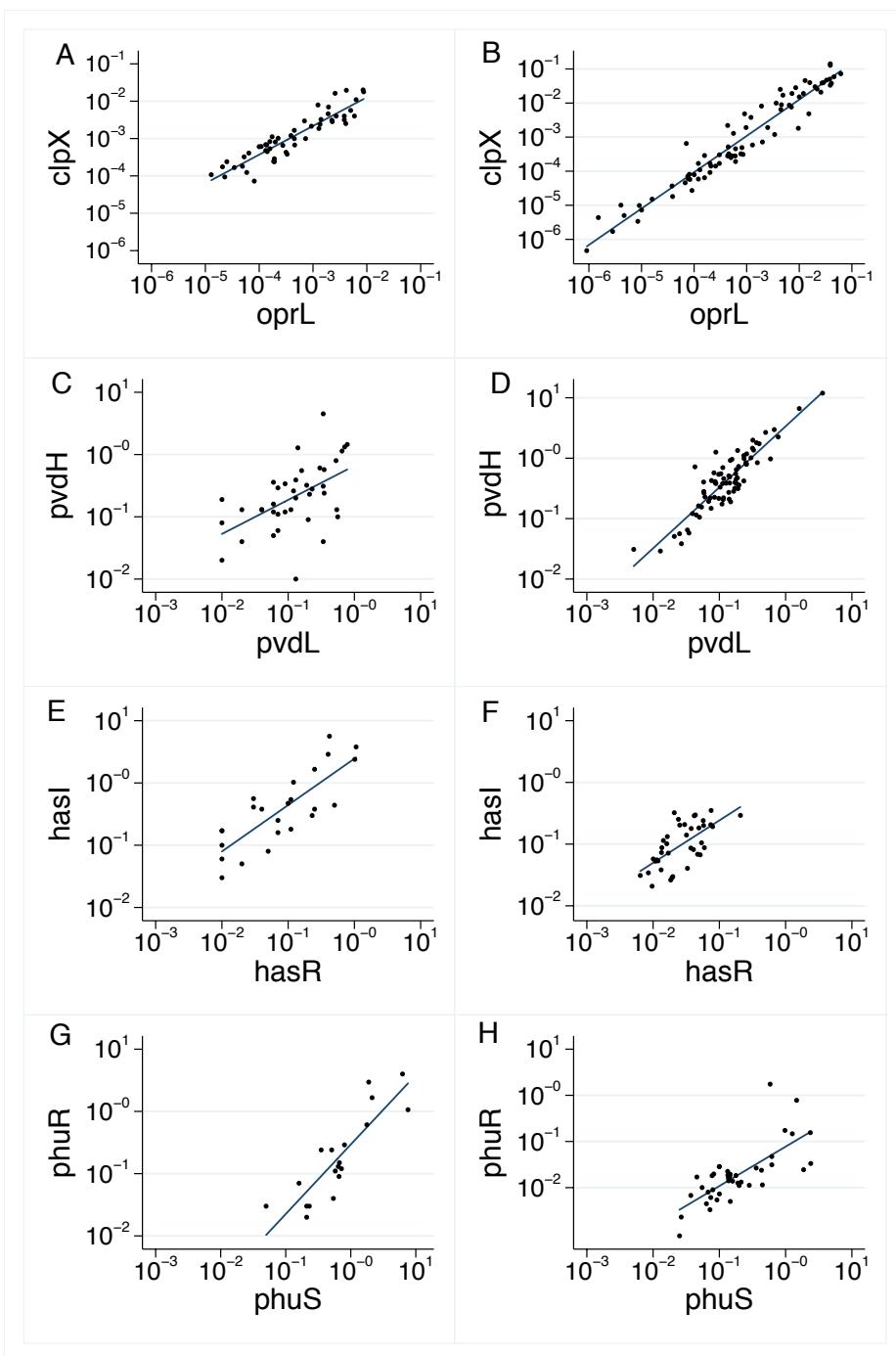


**Table S1.** qPCR primers used in this study.

Target gene	Primers (5' ->3')*	Amplification efficiency†
<i>clpX</i>	GTGGGCGAGGAATGTCGAGAAC, CGGTACCCCTCGATGAGCTTCAG	1.88
<i>oprL</i>	CCAACAGCGGTGCCGTTGA, GCCATATTGTACTCGCGGGT	1.92
<i>pvdH</i>	CAGCACCATCCTGTCGTTCCA, GCAGGTTCGCCTTGACCC	1.87
<i>pvdL</i>	ACCCTGCGTGCTGATGTC, TCGGCTCGGAACCGGAGAA	1.88
<i>pvdS</i>	AGATCACTTCGTCGTTCAAGGCA, GATGTGTTCGAGGGTCGCGTA	1.94
<i>pchF</i>	CTGAGCTTCGACCTCTCGGTCTA, CGGCTCGCTCTCCAGGTA	1.99
<i>hasI</i>	TGGATGCCGATGCGCTTG, CAGCGGGAAATCCTCGAGT	1.85
<i>hasR</i>	GAGAACCAAGGCCTCTGGG, TCGGTCTGGTAGGTGATCGAGT	1.84
<i>phuR</i>	AGCCACTCCTGGTTGACCTC, CGTAGTTCCAGCCCAGCTTG	1.80
<i>phuS</i>	GCGACCTGGCGAAACTCT, GCCAAAGCTCGGCGATGC	1.83
<i>feoB</i>	GATCTTCATCGACGGCATCCAGTG, CAGCGAGAGGAACAGGTACATCA	1.81

\* LightCycler Probe Design Software 2.0 (Roche) was used to design 18-25 bp primers spanning 190 - 210 bp amplicons with a target annealing temperature of 64°C. Several candidate primer pairs for each gene were screened by BLAST [53] against the non-redundant and microbial databases (NCBI) to confirm specificity for the target product and the selected primers are shown.

† Standard curves were constructed with serial dilutions of *P. aeruginosa* PAO1-derived cDNA and analysed with LightCycler 480 software to determine the amplification efficiency for each primer pair.



**Figure S1. Correlation of gene expression in sputum from CF patients.** Correlation of gene expression is shown for *clpX* and *oprL* (A: set 1, B: set 2), *pvdL* and *pvdH* (C: set 1, D: set 2), *hasI* and *hasR* (E: set 1, F: set 2) and *phuR* and *phuS* (G: set 1, H: set 2).